

BC #8



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/914,352

DATE: 01/22/2002

TIME: 10:26:21

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3 <110> APPLICANT: MATTSSON, JENS
 5 <120> TITLE OF INVENTION: MITE PROTEIN
 7 <130> FILE REFERENCE: 53631-65307
 9 <140> CURRENT APPLICATION NUMBER: 09/914,352
 C--> 10 <141> CURRENT FILING DATE: 2001-12-14
 12 <150> PRIOR APPLICATION NUMBER: PCT/SE00/00346
 13 <151> PRIOR FILING DATE: 2000-02-22
 15 <150> PRIOR APPLICATION NUMBER: SE 9900674-4
 16 <151> PRIOR FILING DATE: 1999-02-25
 18 <160> NUMBER OF SEQ ID NOS: 7
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1284
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Sarcoptes scabiei
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (1)..(1281)
 31 <400> SEQUENCE: 1
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 33 Glu Ala Glu Val Thr Phe Ser Asp Ser Glu Asp Lys Lys Asn Tyr Phe
 34 1 5 10 15
 36 gtc gaa ctt aaa aaa gat aaa gat tta tat tcg atg aaa tcg aat gtg 96
 37 Val Glu Leu Lys Lys Asp Lys Asp Leu Tyr Ser Met Lys Ser Asn Val
 38 20 25 30
 40 aaa cga aac aat gag att ttc tat gag aac aat atg gat ttg gag aag 144
 41 Lys Arg Asn Asn Glu Ile Phe Tyr Glu Asn Asn Met Asp Leu Glu Lys
 42 35 40 45
 44 aac ggt aaa atg aat tgg tat tac aaa cga aac gat cga aca tgg aat 192
 45 Asn Gly Lys Met Asn Trp Tyr Tyr Lys Arg Asn Asp Arg Thr Trp Asn
 46 50 55 60
 48 atg gat ctc gat aat gca ttc aat cca aga gat ggt aca atg aaa ctt 240
 49 Met Asp Leu Asp Asn Ala Phe Asn Pro Arg Asp Gly Thr Met Lys Leu
 50 65 70 75 80
 52 caa gtg aaa gat cgt atc tat gat atc aaa ttg aaa cga gaa cgg ttc 288
 53 Gln Val Lys Asp Arg Ile Tyr Asp Ile Lys Leu Lys Arg Glu Arg Phe
 54 85 90 95
 56 cga tac ggt gat cta cat atc gaa gga aat gag aat cct ttg atc aaa 336
 57 Arg Tyr Gly Asp Leu His Ile Glu Gly Asn Glu Asn Pro Leu Ile Lys
 58 100 105 110
 60 aag ggt gat tta cat atg tct ctc gtc gat ccg ctt act ttg aat gtt 384
 61 Lys Gly Asp Leu His Met Ser Leu Val Asp Pro Leu Thr Leu Asn Val
 62 115 120 125

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64 ttg acc aag aat gat gga atc gtc gat atg aca ttg gat ttg gtc tct 432
65 Leu Thr Lys Asn Asp Gly Ile Val Asp Met Thr Leu Asp Leu Val Ser
66      130      135      140
68 ccc aac acc aaa aaa gca gcg cta aaa atc aat tcg aaa aaa tac gat 480
69 Pro Asn Thr Lys Lys Ala Ala Leu Lys Ile Asn Ser Lys Lys Tyr Asp
70 145      150      155      160
72 ctt gat cat gat ggt gag att acc gtt tcg atc ttt aat cct cga atg 528
73 Leu Asp His Asp Gly Glu Ile Thr Val Ser Ile Phe Asn Pro Arg Met
74      165      170      175
76 act tgg aaa cat cac act aga aaa ggt gat atg gaa ttg aat att gat 576
77 Thr Trp Lys His His Thr Arg Lys Gly Asp Met Glu Leu Asn Ile Asp
78      180      185      190
80 gct gat atc act cga aaa ggt tca ttg atc acc tat tct cgt aaa gag 624
81 Ala Asp Ile Thr Arg Lys Gly Ser Leu Ile Thr Tyr Ser Arg Lys Glu
82      195      200      205
84 cca gat gat tcg aca aaa gtt cga tat tca aga caa gga aat caa gtt 672
85 Pro Asp Asp Ser Thr Lys Val Arg Tyr Ser Arg Gln Gly Asn Gln Val
86      210      215      220
88 tcg atg gaa gtc gat tct aaa ttg atc gaa ggc cat gcg aac gga act 720
89 Ser Met Glu Val Asp Ser Lys Leu Ile Glu Gly His Ala Asn Gly Thr
90 225      230      235      240
92 ttg acc gat ggc aaa att cat gtc aaa ggt cga gag agt gat ttc gaa 768
93 Leu Thr Asp Gly Lys Ile His Val Lys Gly Arg Glu Ser Asp Phe Glu
94      245      250      255
96 atc gaa agc acc tat aaa gtt gaa gat ggt aag ctt atg att gag cca 816
97 Ile Glu Ser Thr Tyr Lys Val Glu Asp Gly Lys Leu Met Ile Glu Pro
98      260      265      270
100 acc aaa act cag aat gga aaa tta gaa ggt ctt ctt tcg aga aaa gta 864
101 Thr Lys Thr Gln Asn Gly Lys Leu Glu Gly Leu Leu Ser Arg Lys Val
102      275      280      285
104 cca tca cat ctt gtt ctt gaa aca cca aga gtg aaa atg aac atg aaa 912
105 Pro Ser His Leu Val Leu Glu Thr Pro Arg Val Lys Met Asn Met Lys
106      290      295      300
108 tat gat aga ttt gct ccg gtg aag ata ttg aaa tta gat tac gat ggt 960
109 Tyr Asp Arg Phe Ala Pro Val Lys Ile Leu Lys Leu Asp Tyr Asp Gly
110 305      310      315      320
112 ttg aat tat gag aaa cat atc gat gct gaa tac gag cca tca aat cat 1008
113 Leu Asn Tyr Glu Lys His Ile Asp Ala Glu Tyr Glu Pro Ser Asn His
114      325      330      335
116 tac aaa tac ttt acc gat ggt aaa tcg aag aga agt ggc aaa ggt tat 1056
117 Tyr Lys Tyr Phe Thr Asp Gly Lys Ser Lys Arg Ser Gly Lys Gly Tyr
118      340      345      350
120 tcg atc aaa atc gat gga aaa cca aag aaa gca ttg aaa gtt gat gtc 1104
121 Ser Ile Lys Ile Asp Gly Lys Pro Lys Lys Ala Leu Lys Val Asp Val
122      355      360      365
124 gat atg ccg gat ttt aaa ttc aat gtg aac aaa ccg gaa gat agt aac 1152
125 Asp Met Pro Asp Phe Lys Phe Asn Val Asn Lys Pro Glu Asp Ser Asn
126      370      375      380
128 aaa gct caa ttt agt tat aca ttc aat gat tat acc gaa acg gaa gag 1200

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129 Lys Ala Gln Phe Ser Tyr Thr Phe Asn Asp Tyr Thr Glu Thr Glu Glu
130 385                               390                               395                               400
132 tat gaa ttc gat cca cat cgt gca tat atc ttg aat tgg gcc aga gct 1248
133 Tyr Glu Phe Asp Pro His Arg Ala Tyr Ile Leu Asn Trp Ala Arg Ala
134                               405                               410                               415
136 atc aga caa tat ttg cag aca ttc att gtt gag tag 1284
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138                               420                               425
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142 <211> LENGTH: 427
143 <212> TYPE: PRT
144 <213> ORGANISM: Sarcoptes scabiei
146 <400> SEQUENCE: 2
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148 1 5 10 15
150 Val Glu Leu Lys Lys Asp Lys Asp Leu Tyr Ser Met Lys Ser Asn Val
151 20 25 30
153 Lys Arg Asn Asn Glu Ile Phe Tyr Glu Asn Asn Met Asp Leu Glu Lys
154 35 40 45
156 Asn Gly Lys Met Asn Trp Tyr Tyr Lys Arg Asn Asp Arg Thr Trp Asn
157 50 55 60
159 Met Asp Leu Asp Asn Ala Phe Asn Pro Arg Asp Gly Thr Met Lys Leu
160 65 70 75 80
162 Gln Val Lys Asp Arg Ile Tyr Asp Ile Lys Leu Lys Arg Glu Arg Phe
163 85 90 95
165 Arg Tyr Gly Asp Leu His Ile Glu Gly Asn Glu Asn Pro Leu Ile Lys
166 100 105 110
168 Lys Gly Asp Leu His Met Ser Leu Val Asp Pro Leu Thr Leu Asn Val
169 115 120 125
171 Leu Thr Lys Asn Asp Gly Ile Val Asp Met Thr Leu Asp Leu Val Ser
172 130 135 140
174 Pro Asn Thr Lys Lys Ala Ala Leu Lys Ile Asn Ser Lys Lys Tyr Asp
175 145 150 155 160
177 Leu Asp His Asp Gly Glu Ile Thr Val Ser Ile Phe Asn Pro Arg Met
178 165 170 175
180 Thr Trp Lys His His Thr Arg Lys Gly Asp Met Glu Leu Asn Ile Asp
181 180 185 190
183 Ala Asp Ile Thr Arg Lys Gly Ser Leu Ile Thr Tyr Ser Arg Lys Glu
184 195 200 205
186 Pro Asp Asp Ser Thr Lys Val Arg Tyr Ser Arg Gln Gly Asn Gln Val
187 210 215 220
189 Ser Met Glu Val Asp Ser Lys Leu Ile Glu Gly His Ala Asn Gly Thr
190 225 230 235 240
192 Leu Thr Asp Gly Lys Ile His Val Lys Gly Arg Glu Ser Asp Phe Glu
193 245 250 255
195 Ile Glu Ser Thr Tyr Lys Val Glu Asp Gly Lys Leu Met Ile Glu Pro
196 260 265 270
198 Thr Lys Thr Gln Asn Gly Lys Leu Glu Gly Leu Leu Ser Arg Lys Val
199 275 280 285

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201 Pro Ser His Leu Val Leu Glu Thr Pro Arg Val Lys Met Asn Met Lys
202      290      295      300
204 Tyr Asp Arg Phe Ala Pro Val Lys Ile Leu Lys Leu Asp Tyr Asp Gly
205 305      310      315      320
207 Leu Asn Tyr Glu Lys His Ile Asp Ala Glu Tyr Glu Pro Ser Asn His
208      325      330      335
210 Tyr Lys Tyr Phe Thr Asp Gly Lys Ser Lys Arg Ser Gly Lys Gly Tyr
211      340      345      350
213 Ser Ile Lys Ile Asp Gly Lys Pro Lys Lys Ala Leu Lys Val Asp Val
214      355      360      365
216 Asp Met Pro Asp Phe Lys Phe Asn Val Asn Lys Pro Glu Asp Ser Asn
217      370      375      380
219 Lys Ala Gln Phe Ser Tyr Thr Phe Asn Asp Tyr Thr Glu Thr Glu Glu
220 385      390      395      400
222 Tyr Glu Phe Asp Pro His Arg Ala Tyr Ile Leu Asn Trp Ala Arg Ala
223      405      410      415
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226      420      425
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230 <211> LENGTH: 12
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
236 peptide
238 <400> SEQUENCE: 3
239 Ser Arg Cys Asp Leu Gln His His His His His His
240 1      5      10
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 24
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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255 <210> SEQ ID NO: 5
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257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
263 <400> SEQUENCE: 5      23
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268 <211> LENGTH: 30
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:

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275 <400> SEQUENCE: 6 30
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280 <211> LENGTH: 29
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
287 <400> SEQUENCE: 7 29
288 cgggatccga atatttcgtc tcgaaaccg

VERIFICATION SUMMARY

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